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Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
         35   40   45

Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
      50   55   60

Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65   70   75   80

Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
               85   90   95

Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
            100   105   110

Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
         115   120   125

Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
      130   135   140

His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145   150   155   160

(1/29)

```
Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
            165                 170                 175

Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
            180                 185                 190

Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser
        195                 200                 205

Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
    210                 215                 220

Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225                 230                 235                 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
                245                 250                 255

Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
            260                 265                 270

Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
    275                 280                 285

Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
    290                 295                 300

Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
305                 310                 315                 320

Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg
                325                 330                 335

Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
            340                 345                 350

Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Lys Asp Val Gln Arg
        355                 360                 365

Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Trp
    370                 375                 380

Tyr Thr Val Thr His Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
385                 390                 395                 400

Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
                405                 410                 415

Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
            420                 425                 430

Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
        435                 440                 445

Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
    450                 455                 460

Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
465                 470                 475                 480
                        (2/29)
```

```
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
            485                   490                   495

Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
            500                   505                   510

Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
        515                   520                   525

Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
    530                   535                   540

Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
545                   550                   555                   560

Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
                565                   570                   575

Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
        580                   585                   590

Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
    595                   600                   605

Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
    610                   615                   620

Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
625                   630                   635                   640

Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
                645                   650                   655

Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
                660                   665                   670

Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
        675                   680                   685

Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
    690                   695                   700

Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Glu Phe Leu Val
705                   710                   715                   720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe Leu
                725                   730                   735

Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu
            740                   745                   750

Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu
        755                   760                   765

Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His
    770                   775                   780

Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ser Arg Val Phe
785                   790                   795                   800
                        (3/29)
```

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Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu
              805                 810                     815

Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile
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Arg Asp Ser Val Val
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<212> DNA
<213> Human

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accctgtacg tgggtgctcg agaggccctc tttgcactca gtagcaacct cagcttcctg    300

ccaggcgggg agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc    360

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aactttctca aggaccactt cctgatggac gggcaggtcc gaagccgcat gctgctgctg   1320
```

                                    (4/29)

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<211> 3766
<212> DNA
<213> Human

<400> 3

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agtccggccg agccacctga gcccgagccg cgggacaccg tcgctcctgc tctccgaatg    240

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              20                  25                  30

Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
            35                  40                  45

Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
    50                  55                  60

Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65                  70                  75                  80

Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
                85                  90                  95

Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
            100                 105                 110

Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
        115                 120                 125

Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
    130                 135                 140

His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145                 150                 155                 160

Ile Asn Met Glu Asp Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
            165                 170                 175

Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
        180                 185                 190

Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ile
    195                 200                 205

Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
    210                 215                 220

Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225                 230                 235                 240

Val Ala Ser Ala Tyr Ile Glu Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
            245                 250                 255

Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
        260                 265                 270

Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
    275                 280                 285

Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
290                 295                 300

Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
305                 310                 315                 320

Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg
            325                 330                 335
```

(8/29)

```
Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
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Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Lys Asp Val Gln Arg
            355                 360                 365

Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Trp
    370                 375                 380

Tyr Thr Val Thr His Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
385                 390                 395                 400

Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
            405                 410                 415

Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
            420                 425                 430

Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
            435                 440                 445

Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
    450                 455                 460

Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
465                 470                 475                 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
            485                 490                 495

Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
            500                 505                 510

Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
            515                 520                 525

Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
            530                 535                 540

Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
545                 550                 555                 560

Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
            565                 570                 575

Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
            580                 585                 590

Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
            595                 600                 605

Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
    610                 615                 620

Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
625                 630                 635                 640

Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
            645                 650                 655
                            (9/29)
```

```
Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
            660                 665                 670

Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
        675                 680                 685

Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
    690                 695                 700

Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
705                 710                 715                 720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe Leu
            725                 730                 735

Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu
            740                 745                 750

Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu
        755                 760                 765

Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His
    770                 775                 780

Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ser Arg Val Phe
785                 790                 795                 800

Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu
            805                 810                 815

Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile
            820                 825                 830

Arg Asp Ser Val Val
            835

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<212> DNA
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(10/29)

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caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga cccagctttt    720

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(11/29)

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                                (12/29)

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Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
        35   40   45

Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
    50   55   60

Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65   70   75   80

Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
                85   90   95

Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
            100   105   110

Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
            115   120   125

Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
        130   135   140

His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145   150   155   160

Ile Asn Ile Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
                165   170   175

Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
            180   185   190

                                (14/29)
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Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
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Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225                 230                 235                 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
            245                 250                 255

Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
        260                 265                 270

Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
    275                 280                 285

Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
    290                 295                 300

Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
305                 310                 315                 320

Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg
            325                 330                 335

Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
        340                 345                 350

Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Lys Asp Val Gln Arg
    355                 360                 365

Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Trp
    370                 375                 380

Tyr Thr Val Thr His Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
385                 390                 395                 400

Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
            405                 410                 415

Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
        420                 425                 430

Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
    435                 440                 445

Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
    450                 455                 460

Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
465                 470                 475                 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
            485                 490                 495

Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
        500                 505                 510

(15/29)

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Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
        515                 520                 525

Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
    530                 535                 540

Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
545                 550                 555                 560

Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
            565                 570                 575

Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
        580                 585                 590

Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
        595                 600                 605

Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
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Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
625                 630                 635                 640

Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
            645                 650                 655

Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
            660                 665                 670

Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
        675                 680                 685

Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
    690                 695                 700

Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
705                 710                 715                 720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Pro Leu
            725                 730                 735

Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu
            740                 745                 750

Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu
        755                 760                 765

Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His
    770                 775                 780

Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ser Arg Val Phe
785                 790                 795                 800

Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu
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Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile
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                            (16/29)
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(17/29)

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gtcctctccc cagtcccag ttcaccctcc atccctcacc ttcctccact ctaaggggata   3660

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<210> 10
<211> 837
<212> PRT
<213> Human

<400> 10
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Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu Leu
            20                  25                  30

Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
        35                  40                  45
```

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Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
    50                  55                      60

Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65                  70                  75                      80

Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
                85                  90                  95

Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
            100                 105                 110

Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
        115                 120                 125

Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
    130                 135                 140

His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145                 150                 155                 160

Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
            165                 170                 175

Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
            180                 185                 190

Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser
        195                 200                 205

Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
    210                 215                 220

Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225                 230                 235                 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
            245                 250                 255

Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
        260                 265                 270

Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
    275                 280                 285

Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
    290                 295                 300

Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
305                 310                 315                 320

Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg
            325                 330                 335

Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
        340                 345                 350

Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Asn Asp Val Gln Arg
    355                 360                 365
```

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```
Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Trp
    370                 375                 380

Tyr Thr Val Thr His Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
385                 390                 395                 400

Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
                405                 410                 415

Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
            420                 425                 430

Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
        435                 440                 445

Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
    450                 455                 460

Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
465                 470                 475                 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
                485                 490                 495

Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
            500                 505                 510

Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
        515                 520                 525

Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
    530                 535                 540

Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
545                 550                 555                 560

Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
            565                 570                 575

Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
        580                 585                 590

Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
        595                 600                 605

Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
    610                 615                 620

Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
625                 630                 635                 640

Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
            645                 650                 655

Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
        660                 665                 670

Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
    675                 680                 685
                          (22/29)
```

```
Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
    690                 695                 700

Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
705                 710                 715                 720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe Leu
                725                 730                 735

Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu
                740                 745                 750

Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu
        755                 760                 765

Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His
770                 775                 780

Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ser Arg Val Phe
785                 790                 795                 800

Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu
                805                 810                 815

Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile
                820                 825                 830

Arg Asp Ser Val Val
        835

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<211> 2511
<212> DNA
<213> Human

<400> 11
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acctgggcgc tcagcccccg gatcagcctg cctctgggct ctgaagagcg gccattcctc   180

agattcgaag ctgaacacat ctccaactac acagcccttc tgctgagcag ggatggcagg   240

accctgtacg tgggtgctcg agaggccctc tttgcactca gtagcaacct cagcttcctg   300

ccaggcgggg agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc   360

agcttcaagg gcaaggaccc acagcgcgac tgtcaaaact acatcaagat cctcctgccg   420

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atcaacatgg agaacttcac cctggcaagg gacgagaagg ggaatgtcct cctggaagat   540

ggcaagggcc gttgtccctt cgacccgaat ttcaagtcca ctgccctggt ggttgatggc   600

gagctctaca ctggaacagt cagcagcttc caagggaatg acccggccat ctcgcggagc   660

caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga cccagctttt   720
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(23/29)

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acctccttcc tcaaggccca gctgctgtgc tcacggcccg acgatggctt ccccttcaac    960

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tatggggtct tcacttccca gtggcacagg ggaactacag aaggctctgc cgtctgtgtc    1080

ttcacaatga atgatgtgca gagagtcttc agcggcctct acaaggaggt gaaccgtgag    1140

acacagcagt ggtacaccgt gacccacccg gtgcccacac cccggcctgg agcgtgcatc    1200

accaacagtg cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg    1260

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(24/29)

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<211> 3766
<212> DNA
<213> Human

<400> 12
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ctgcgcaccg cgatgggcct gaggagctgg ctcgccgccc catgggcgc gctgccgcct   300

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                                (25/29)

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tggcctcttc accttccaca ttatcccgct gccaccggct gccctgtctc actgcagatt  3240

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ctgccgtcgt cccaccacct cagggaccag agggctaggt tggcactgcg gccctcacca  3360

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ccaccatatc caccctcgct ccatctttga actcaaacac gaggaactaa ctgcaccctg     3600

gtcctctccc cagtccccag ttcaccctcc atccctcacc ttcctccact ctaagggata     3660

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<213> Artificial Sequence

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<223> Oligonucleotide

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<210> 14
<211> 20
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<220>
<223> Oligonucleotide

<400> 14
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<210> 15
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<212> DNA
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<220>
<223> Oligonucleotide

<400> 15
caacaactac atcctcggct                                                    20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 16
tcggctccta catcaacaac                                                    20

<210> 17
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<212> DNA
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<213> Artificial Sequence

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<400> 17
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<210> 18
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<220>
<223> Primer

<400> 18
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<212> DNA
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<220>
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<220>
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<210> 21
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<212> DNA
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<220>
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<210> 23
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<212> PRT
<213> Human

<400> 23
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<210> 24
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<212> PRT
<213> Human

<400> 24
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                5   10   15

<210> 25
<211> 14
<212> PRT
<213> Human

<400> 25
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